



GFI-108 Sequence listing.ST25
SEQUENCE LISTING

<110> GlycoFi, Inc.
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Davidson, Robert C.

<120> N-Acetylglucosaminyltransferase III expression in lower eukaryotes

<130> GFI-108 CIP

<140> US 10/680,963
<141> 2003-10-07

<150> US 10/371,877
<151> 2003-02-20

<150> US 09/892,591
<151> 2001-06-27

<150> US 60/214,358
<151> 2000-06-28

<150> US 60/215,638
<151> 2000-06-30

<150> US 60/279,997
<151> 2001-03-30

<150> PCT/US02/41510
<151> 2002-12-24

<150> US 60/344,169
<151> 2001-12-27

<160> 101

<170> PatentIn version 3.2

<210> 1
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<210> 2
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<210> 3
<211> 21
<212> DNA
<213> artificial

<220>
<223> Primer A for target gene in P. pastoris (1,6-mannosyltransferase)

<400> 3

atggcgaagg cagatggcag t

<210> 4
 <211> 21
 <212> DNA
 <213> artificial

<220>
 <223> Primer B for target gene in P. pastoris (1,6-mannosyltransferase)

<400> 4
 ttagtccttc caacttcctt c

<210> 5
 <211> 26
 <212> DNA
 <213> artificial

<220>
 <223> Primer A for target gene in P. pastoris (1,2
 mannosyltransferases)

<220>
 <221> misc_feature
 <222> (9)..(9)
 <223> wherein "n" is equal to "a" or "t" or "g" or "c".

<220>
 <221> misc_feature
 <222> (12)..(12)
 <223> wherein "n" is equal to "a" or "t" or "g" or "c".

<220>
 <221> misc_feature
 <222> (18)..(18)
 <223> wherein "n" is equal to "a" or "t" or "g" or "c".

<400> 5
 taytggmngn tngarcynga yathaa

<210> 6
 <211> 20
 <212> DNA
 <213> artificial

<220>
 <223> Primer B for target gene in P. pastoris (1,2
 mannosyltransferases)

<220>
 <221> misc_feature
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<220>
 <221> misc_feature
 <222> (12)..(12)
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gcrtcncccc anckytcrt

20

<210> 7
<400> 7
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<210> 8
<400> 8
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<210> 9
<211> 458
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 9

Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys
1 5 10 15

Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly
20 25 30

Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
35 40 45

Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
50 55 60

Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
65 70 75 80

Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
85 90 95

Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
100 105 110

Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
115 120 125

Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
130 135 140

Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
145 150 155 160

Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
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165

170

175

Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
 180 185 190

Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
 195 200 205

Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
 210 215 220

Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
 225 230 235 240

Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
 245 250 255

Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
 260 265 270

His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
 275 280 285

Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His
 290 295 300

Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val
 305 310 315 320

Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
 325 330 335

Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile
 340 345 350

Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg
 355 360 365

Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile
 370 375 380

Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr
 385 390 395 400

Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala
 405 410 415

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Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu Leu Leu Leu Ala
420 425 430

Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg
435 440 445

Thr Thr Ser Ser Met Glu Lys Lys Leu Asn
450 455

<210> 10
<211> 458
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 10

Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys
1 5 10 15

Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly
20 25 30

Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
35 40 45

Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
50 55 60

Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
65 70 75 80

Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
85 90 95

Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
100 105 110

Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
115 120 125

Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
130 135 140

Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
145 150 155 160

Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
165 170 175

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Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
 180 185 190

Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
 195 200 205

Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
 210 215 220

Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
 225 230 235 240

Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
 245 250 255

Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
 260 265 270

His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
 275 280 285

Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His
 290 295 300

Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val
 305 310 315 320

Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
 325 330 335

Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile
 340 345 350

Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg
 355 360 365

Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile
 370 375 380

Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr
 385 390 395 400

Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala
 405 410 415

Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu Leu Leu Leu Ala
 420 425 430

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Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg
435 440 445

Thr Thr Ser Ser Met Glu Lys Lys Leu Asn
450 455

<210> 11
<211> 389
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 11

Trp Gln Asp Leu Lys Asp Gly Val Arg Tyr Val Ile Phe Asp Cys Arg
1 5 10 15

Ala Asn Leu Ile Val Met Pro Leu Leu Ile Leu Phe Glu Ser Met Leu
20 25 30

Cys Lys Ile Ile Ile Lys Lys Val Ala Tyr Thr Glu Ile Asp Tyr Lys
35 40 45

Ala Tyr Met Glu Gln Ile Glu Met Ile Gln Leu Asp Gly Met Leu Asp
50 55 60

Tyr Ser Gln Val Ser Gly Gly Thr Gly Pro Leu Val Tyr Pro Ala Gly
65 70 75 80

His Val Leu Ile Tyr Lys Met Met Tyr Trp Leu Thr Glu Gly Met Asp
85 90 95

His Val Glu Arg Gly Gln Val Phe Phe Arg Tyr Leu Tyr Leu Leu Thr
100 105 110

Leu Ala Leu Gln Met Ala Cys Tyr Tyr Leu Leu His Leu Pro Pro Trp
115 120 125

Cys Val Val Leu Ala Cys Leu Ser Lys Arg Leu His Ser Ile Tyr Val
130 135 140

Leu Arg Leu Phe Asn Asp Cys Phe Thr Thr Leu Phe Met Val Val Thr
145 150 155 160

Val Leu Gly Ala Ile Val Ala Ser Arg Cys His Gln Arg Pro Lys Leu
165 170 175

Lys Lys Ser Leu Ala Leu Val Ile Ser Ala Thr Tyr Ser Met Ala Val
180 185 190

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Ser Ile Lys Met Asn Ala Leu Leu Tyr Phe Pro Ala Met Met Ile Ser
195 200 205

Leu Phe Ile Leu Asn Asp Ala Asn Val Ile Leu Thr Leu Leu Asp Leu
210 215 220

Val Ala Met Ile Ala Trp Gln Val Ala Val Ala Val Pro Phe Leu Arg
225 230 235 240

Ser Phe Pro Gln Gln Tyr Leu His Cys Ala Phe Asn Phe Gly Arg Lys
245 250 255

Phe Met Tyr Gln Trp Ser Ile Asn Trp Gln Met Met Asp Glu Glu Ala
260 265 270

Phe Asn Asp Lys Arg Phe His Leu Ala Leu Leu Ile Ser His Leu Ile
275 280 285

Ala Leu Thr Thr Leu Phe Val Thr Arg Tyr Pro Arg Ile Leu Pro Asp
290 295 300

Leu Trp Ser Ser Leu Cys His Pro Leu Arg Lys Asn Ala Val Leu Asn
305 310 315 320

Ala Asn Pro Ala Lys Thr Ile Pro Phe Val Leu Ile Ala Ser Asn Phe
325 330 335

Ile Gly Val Leu Phe Ser Arg Ser Leu His Tyr Gln Phe Leu Ser Trp
340 345 350

Tyr His Trp Thr Leu Pro Ile Leu Ile Phe Trp Ser Gly Met Pro Phe
355 360 365

Phe Val Gly Pro Ile Trp Tyr Val Leu His Glu Trp Cys Trp Asn Ser
370 375 380

Tyr Pro Pro Asn Ser
385

<210> 12
<211> 375
<212> PRT
<213> Homo sapiens

<400> 12

Trp Gln Glu Arg Arg Leu Leu Leu Arg Glu Pro Arg Tyr Thr Leu Leu
1 5 10 15

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Val Ala Ala Cys Leu Cys Leu Ala Glu Val Gly Ile Thr Phe Trp Val
20 25 30

Ile His Arg Val Ala Tyr Thr Glu Ile Asp Trp Lys Ala Tyr Met Ala
35 40 45

Glu Val Glu Gly Val Ile Asn Gly Thr Tyr Asp Tyr Thr Gln Leu Gln
50 55 60

Gly Asp Thr Gly Pro Leu Val Tyr Pro Ala Gly Phe Val Tyr Ile Phe
65 70 75 80

Met Gly Leu Tyr Tyr Ala Thr Ser Arg Gly Thr Asp Ile Arg Met Ala
85 90 95

Gln Asn Ile Phe Ala Val Leu Tyr Leu Ala Thr Leu Leu Val Phe
100 105 110

Leu Ile Tyr His Gln Thr Cys Lys Val Pro Pro Phe Val Phe Phe
115 120 125

Met Cys Cys Ala Ser Tyr Arg Val His Ser Ile Phe Val Leu Arg Leu
130 135 140

Phe Asn Asp Pro Val Ala Met Val Leu Leu Phe Leu Ser Ile Asn Leu
145 150 155 160

Leu Leu Ala Gln Arg Trp Gly Trp Gly Cys Cys Phe Phe Ser Leu Ala
165 170 175

Val Ser Val Lys Met Asn Val Leu Leu Phe Ala Pro Gly Leu Leu Phe
180 185 190

Leu Leu Leu Thr Gln Phe Gly Phe Arg Gly Ala Leu Pro Lys Leu Gly
195 200 205

Ile Cys Ala Gly Leu Gln Val Val Leu Gly Leu Pro Phe Leu Leu Glu
210 215 220

Asn Pro Ser Gly Tyr Leu Ser Arg Ser Phe Asp Leu Gly Arg Gln Phe
225 230 235 240

Leu Phe His Trp Thr Val Asn Trp Arg Phe Leu Pro Glu Ala Leu Phe
245 250 255

Leu His Arg Ala Phe His Leu Ala Leu Leu Thr Ala His Leu Thr Leu
260 265 270

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Leu Leu Leu Phe Ala Leu Cys Arg Trp His Arg Thr Gly Glu Ser Ile
275 280 285

Leu Ser Leu Leu Arg Asp Pro Ser Lys Arg Lys Val Pro Pro Gln Pro
290 295 300

Leu Thr Pro Asn Gln Ile Val Ser Thr Leu Phe Thr Ser Asn Phe Ile
305 310 315 320

Gly Ile Cys Phe Ser Arg Ser Leu His Tyr Gln Phe Tyr Val Trp Tyr
325 330 335

Phe His Thr Leu Pro Tyr Leu Leu Trp Ala Met Pro Ala Arg Trp Leu
340 345 350

Thr His Leu Leu Arg Leu Leu Val Leu Gly Leu Ile Glu Leu Ser Trp
355 360 365

Asn Thr Tyr Pro Ser Thr Ser
370 375

<210> 13
<211> 271
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 13

Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
1 5 10 15

Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
20 25 30

Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
35 40 45

Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
50 55 60

Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
65 70 75 80

Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
85 90 95

Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
100 105 110

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Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
115 120 125

Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
130 135 140

Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
145 150 155 160

Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
165 170 175

Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
180 185 190

Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
195 200 205

Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
210 215 220

Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
225 230 235 240

His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
245 250 255

Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe
260 265 270

<210> 14

<211> 258

<212> PRT

<213> Drosophila virilis

<400> 14

Ile Lys Tyr Leu Ala Phe Glu Pro Ala Ala Leu Pro Ile Val Ser Val
1 5 10 15

Leu Ile Val Leu Ala Glu Ala Val Ile Asn Val Leu Val Ile Gln Arg
20 25 30

Val Pro Tyr Thr Glu Ile Asp Trp Lys Ala Tyr Met Gln Glu Cys Glu
35 40 45

Gly Phe Leu Asn Gly Thr Thr Asn Tyr Ser Leu Leu Arg Gly Asp Thr
50 55 60

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Gly Pro Leu Val Tyr Pro Ala Ala Phe Val Tyr Ile Tyr Ser Gly Leu
65 70 75 80

Tyr Tyr Leu Thr Gly Gln Gly Thr Asn Val Arg Leu Ala Gln Tyr Ile
85 90 95

Phe Ala Cys Ile Tyr Leu Leu Gln Met Cys Leu Val Leu Arg Leu Tyr
100 105 110

Thr Lys Ser Arg Lys Val Pro Pro Tyr Val Leu Val Leu Ser Ala Phe
115 120 125

Thr Ser Tyr Arg Ile His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp
130 135 140

Pro Val Ala Ile Leu Leu Leu Tyr Ala Ala Leu Asn Leu Phe Leu Asp
145 150 155 160

Gln Arg Trp Thr Leu Gly Ser Ile Cys Tyr Ser Leu Ala Val Gly Val
165 170 175

Lys Met Asn Ile Leu Leu Phe Ala Pro Ala Leu Leu Leu Phe Tyr Leu
180 185 190

Ala Asn Leu Gly Val Leu Arg Thr Leu Val Gln Leu Thr Ile Cys Ala
195 200 205

Val Leu Gln Leu Phe Ile Gly Ala Pro Phe Leu Arg Thr His Pro Met
210 215 220

Glu Tyr Leu Arg Gly Ser Phe Asp Leu Gly Arg Ile Phe Glu His Lys
225 230 235 240

Trp Thr Val Asn Tyr Arg Phe Leu Ser Lys Glu Leu Phe Glu Gln Arg
245 250 255

Glu Phe

<210> 15
<211> 60
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 15

Ile Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser
1 5 10 15

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Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro
20 25 30

Ile Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp
35 40 45

Tyr Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro
50 55 60

<210> 16

<211> 58

<212> PRT

<213> Drosophila virilis

<400> 16

Leu Pro Phe Phe Leu Cys Asn Phe Ile Gly Val Ala Cys Ala Arg Ser
1 5 10 15

Leu His Tyr Gln Phe Tyr Ile Trp Tyr Phe His Ser Leu Pro Tyr Leu
20 25 30

Val Trp Ser Thr Pro Tyr Ser Leu Gly Val Arg Tyr Leu Ile Leu Gly
35 40 45

Ile Ile Glu Tyr Cys Trp Asn Thr Tyr Pro
50 55

<210> 17

<211> 270

<212> PRT

<213> Saccharomyces cerevisiae

<400> 17

Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro Leu
1 5 10 15

Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys Val
20 25 30

Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu Met
35 40 45

Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly Thr
50 55 60

Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met Met
65 70 75 80

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Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val Phe
85 90 95

Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys Tyr
100 105 110

Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu Ser
115 120 125

Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys Phe
130 135 140

Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala Ser
145 150 155 160

Arg Cys His Gln Arg Pro Lys Leu Lys Ser Leu Ala Leu Val Ile
165 170 175

Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu Leu
180 185 190

Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala Asn
195 200 205

Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln Val
210 215 220

Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu His
225 230 235 240

Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile Asn
245 250 255

Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe
260 265 270

<210> 18
<211> 257
<212> PRT
<213> Drosophila melanogaster

<400> 18

Lys Tyr Leu Leu Leu Glu Pro Ala Ala Leu Pro Ile Val Gly Leu Phe
1 5 10 15

Val Leu Leu Ala Glu Leu Val Ile Asn Val Val Val Ile Gln Arg Val
20 25 30

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Pro Tyr Thr Glu Ile Asp Trp Val Ala Tyr Met Gln Glu Cys Glu Gly
35 40 45

Phe Leu Asn Gly Thr Thr Asn Tyr Ser Leu Leu Arg Gly Asp Thr Gly
50 55 60

Pro Leu Val Tyr Pro Ala Ala Phe Val Tyr Ile Tyr Ser Ala Leu Tyr
65 70 75 80

Tyr Val Thr Ser His Gly Thr Asn Val Arg Leu Ala Gln Tyr Ile Phe
85 90 95

Ala Gly Ile Tyr Leu Leu Gln Leu Ala Leu Val Leu Arg Leu Tyr Ser
100 105 110

Lys Ser Arg Lys Val Pro Pro Tyr Val Leu Val Leu Ser Ala Phe Thr
115 120 125

Ser Tyr Arg Ile His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Pro
130 135 140

Val Ala Val Leu Leu Leu Tyr Ala Ala Leu Asn Leu Phe Leu Asp Arg
145 150 155 160

Arg Trp Thr Leu Gly Ser Thr Phe Phe Ser Leu Ala Val Gly Val Lys
165 170 175

Met Asn Ile Leu Leu Phe Ala Pro Ala Leu Leu Leu Phe Tyr Leu Ala
180 185 190

Asn Leu Gly Leu Leu Arg Thr Ile Leu Gln Leu Ala Val Cys Gly Val
195 200 205

Ile Gln Leu Leu Leu Gly Ala Pro Phe Leu Leu Thr His Pro Val Glu
210 215 220

Tyr Leu Arg Gly Ser Phe Asp Leu Gly Arg Ile Phe Glu His Lys Trp
225 230 235 240

Thr Val Asn Tyr Arg Phe Leu Ser Arg Asp Val Phe Glu Asn Arg Thr
245 250 255

Phe

<210> 19

<211> 60

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<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 19

Ile Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser
1 5 10 15

Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro
20 25 30

Ile Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp
35 40 45

Tyr Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro
50 55 60

<210> 20

<211> 58

<212> PRT

<213> *Drosophila melanogaster*

<400> 20

Leu Pro Phe Phe Leu Cys Asn Leu Val Gly Val Ala Cys Ser Arg Ser
1 5 10 15

Leu His Tyr Gln Phe Tyr Val Trp Tyr Phe His Ser Leu Pro Tyr Leu
20 25 30

Ala Trp Ser Thr Pro Tyr Ser Leu Gly Val Arg Cys Leu Ile Leu Gly
35 40 45

Leu Ile Glu Tyr Cys Trp Asn Thr Tyr Pro
50 55

<210> 21

<211> 1377

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 21

atggaaggta aacagtctcc gcaaggtaa aagtctctgc aaaggaagca atttgcaga 60

cctccgctgg atctgtggca ggatctcaag gacgggtgc gctacgtgat cttcgattgt 120

agggccaatc ttatcgttat gcccctttg atttgttcg aaagcatgct gtgcaagatt 180

atcattaaga aggttagctt cacagagatc gattacaagg cgtacatgga gcagatcgag 240

atgattcagc tcgatggcat gctggactac tctcaggta gtgggtgaac gggccgctg 300

gtgtatccag caggccacgt cttgatctac aagatgtatgt actggctaag agagggatg 360

gaccacgttgc agcgcggca agtgttttc agatacttgtt atctccttac actggcgtt 420

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caaatggcgt gttactacct	tttacatcta ccaccgtgg	gtgtggtctt ggcgtgcctc	480
tctaaaagat tgcactctat	ttacgtgcta cggttattca	atgattgctt cactacttg	540
tttatggtcg tcacggttt	ggggctatc gtggccagca	ggtgccatca gcgc(cc)aaa	600
ttaaagaagt cccttgcgt	ggtgatctcc gcaacataca	gtatggctgt gagcattaag	660
atgaatgcgc tgggtat	tttccctgcaatg atgatttctc	tattcatctt taatgacgcg	720
aacgtaatcc ttacttgtt	ggatctcggtt gcgatgattt	catggcaagt cgca(g)ttgca	780
gtgc(cc)ttcc tgcgca	ttccgcacag tacctgcatt	g(c)gc(ttt)aa ttccggcagg	840
aagtttatgt accaatggag	tatcaattgg caaatgatgg	atgaagaggc tttcaatgat	900
aagagggtcc acttggccct	tttaatcagc cacctgatag	cgctcaccac actgttcgtc	960
acaagatacc ctcgcac	cttgcatttta tggcttccc	tgtgccatcc gctgaggaaa	1020
aatgcagtgc tcaatgcca	tcccgccaag actattccat	tcgttcta(c)at cgcatccaac	1080
ttcatcgccg tcctat	tttc aaggccctc cactaccat	gtatcacttg	1140
actttgccta tactgat	tttctt ttggcgggaa atgccc	tcgttggtcc catttggtac	1200
gtcttgcacg agtggtgct	gaattccat ccaccaaact	cacaagcaag cacgctattt	1260
ttggcattga atactgtt	tttctt cttga cgca	gctatc tggttcggtc	1320
gccctcgcca aaagccat	tcgttaccacc agctctatgg	aaaaaaagct caactga	1377

<210> 22

<211> 458

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 22

Met	Glu	Gly	Glu	Gln	Ser	Pro	Gln	Gly	Glu	Lys	Ser	Leu	Gln	Arg	Lys
1				5				10				15			

Gln	Phe	Val	Arg	Pro	Pro	Leu	Asp	Leu	Trp	Gln	Asp	Leu	Lys	Asp	Gly
				20				25				30			

Val	Arg	Tyr	Val	Ile	Phe	Asp	Cys	Arg	Ala	Asn	Leu	Ile	Val	Met	Pro
				35			40				45				

Leu	Leu	Ile	Leu	Phe	Glu	Ser	Met	Leu	Cys	Lys	Ile	Ile	Ile	Lys	Lys
				50			55			60					

Val	Ala	Tyr	Thr	Glu	Ile	Asp	Tyr	Lys	Ala	Tyr	Met	Glu	Gln	Ile	Glu
65				70				75			80				

Met	Ile	Gln	Leu	Asp	Gly	Met	Leu	Asp	Tyr	Ser	Gln	Val	Ser	Gly	Gly
				85				90			95				

GFI-108 Sequence listing.ST25

Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
100 105 110

Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
115 120 125

Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
130 135 140

Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
145 150 155 160

Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
165 170 175

Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
180 185 190

Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
195 200 205

Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
210 215 220

Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
225 230 235 240

Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
245 250 255

Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
260 265 270

His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
275 280 285

Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His
290 295 300

Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val
305 310 315 320

Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
325 330 335

Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile
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GFI-108 Sequence listing, ST25

340

345

350

Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg
 355 360 365

Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile
 370 375 380

Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr
 385 390 395 400

Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala
 405 410 415

Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu Leu Leu Leu Ala
 420 425 430

Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg
 435 440 445

Thr Thr Ser Ser Met Glu Lys Lys Leu Asn
 450 455

<210> 23
 <211> 1395

<212> DNA

<213> Pichia pastoris

<400> 23		
atgcctccga tagagccagc taaaaaggcca aagcttacgc taaaaatgt tatcggtgat	60	
ctagtggctc ttattcaaaa cgttttattt aacccagatt ttagtgtctt cggtgcacct	120	
cttttatggt tagctgattc cattgttac aaggtgatca ttggcactgt ttcctacaca	180	
gatattgatt tttcttcata tatgcaacaa atctttaaaa ttcgacaagg agaatttagat	240	
tatagcaaca tatttggta caccggcca ttggtttacc cagccggcca tggatgttgc	300	
tactcagtttac ttccgtggta cagtatgggt ggagaagacg tcagttcgt tcaacaagca	360	
tttgggttgt tatacctagg ttgcttggta ctatccatca gctcctactt tttctctggc	420	
tttagggaaaa tacctccggt ttatgttgc ttgttgttag cgtccaaagag actgcattca	480	
atatttgtat tgagactctt caatgactgt ttaacaacat tttgtatgtt ggcaactata	540	
atcatcccttc aacaagcaag tagctggagg aaagatggca caactattcc attatctgc	600	
cctgatgctg cagatacgtt cagtttagcc atctctgtaa agatgaatgc gctgctatac	660	
ctcccagcat tcctactact catatatctc atttgtgacg aaaatttgat taaaggcattg	720	
gcacccgttc tagtttgat attggtgcaa gtaggagtcg gttattcggtt cattttaccg	780	

GFI-108 Sequence listing.ST25

ttgcactatg atgatcaggc aaatgaaatt cgttctgcct acttagaca ggctttgac	840
tttagtcgcc aatttctta taagtggacg gttattggc gcttttgag ccaagaaact	900
ttcaacaatg tccatttca ccagctcctg tttgctctcc atattattac gttagtcttgc	960
ttcatcctca agttcctctc tcctaaaaac attggaaaac cgcttggtag atttgtgttgc	1020
gacatttca aattttggaa gccaacctta tctccaacca atattatcaa cgacccagaa	1080
agaagcccgat attttgttta caccgtcatg gctactacca acttaatagg ggtgcttttgc	1140
gcaagatctt tacactacca gttcctaagc tggtatgcgt tctcttgcc atatctccttgc	1200
tacaaggctc gtctgaacctt tatagcatct attattgttt atgcccgtca cgagtattgc	1260
tggttggttt tcccagctac agaacaaagt tccgcgttgt tggtatctat cttactacttgc	1320
atcctgatttc tcattttac caacgaacag ttatccctt ctcaatcggt ccctgcagaa	1380
aaaaagaata cataa	1395

<210> 24

<211> 464

<212> PRT

<213> *Pichia pastoris*

<400> 24

Met Pro Pro Ile Glu Pro Ala Glu Arg Pro Lys Leu Thr Leu Lys Asn
 1 5 10 15

Val Ile Gly Asp Leu Val Ala Leu Ile Gln Asn Val Leu Phe Asn Pro
 20 25 30

Asp Phe Ser Val Phe Val Ala Pro Leu Leu Trp Leu Ala Asp Ser Ile
 35 40 45

Val Ile Lys Val Ile Ile Gly Thr Val Ser Tyr Thr Asp Ile Asp Phe
 50 55 60

Ser Ser Tyr Met Gln Gln Ile Phe Lys Ile Arg Gln Gly Glu Leu Asp
 65 70 75 80

Tyr Ser Asn Ile Phe Gly Asp Thr Gly Pro Leu Val Tyr Pro Ala Gly
 85 90 95

His Val His Ala Tyr Ser Val Leu Ser Trp Tyr Ser Asp Gly Gly Glu
 100 105 110

Asp Val Ser Phe Val Gln Gln Ala Phe Gly Trp Leu Tyr Leu Gly Cys
 115 120 125

Leu Leu Leu Ser Ile Ser Ser Tyr Phe Phe Ser Gly Leu Gly Lys Ile

135 GFI-108 Sequence listing.ST25
140

Pro Pro Val Tyr Phe Val Leu Leu Val Ala Ser Lys Arg Leu His Ser
 145 150 155 160
 Ile Phe Val Leu Arg Leu Phe Asn Asp Cys Leu Thr Thr Phe Leu Met
 165 170 175
 Leu Ala Thr Ile Ile Leu Gln Gln Ala Ser Ser Trp Arg Lys Asp
 180 185 190
 Gly Thr Thr Ile Pro Leu Ser Val Pro Asp Ala Ala Asp Thr Tyr Ser
 195 200 205
 Leu Ala Ile Ser Val Lys Met Asn Ala Leu Leu Tyr Leu Pro Ala Phe
 210 215 220
 Leu Leu Leu Ile Tyr Leu Ile Cys Asp Glu Asn Leu Ile Lys Ala Leu
 225 230 235 240
 Ala Pro Val Leu Val Leu Ile Leu Val Gln Val Gly Val Gly Tyr Ser
 245 250 255
 Phe Ile Leu Pro Leu His Tyr Asp Asp Gln Ala Asn Glu Ile Arg Ser
 260 265 270
 Ala Tyr Phe Arg Gln Ala Phe Asp Phe Ser Arg Gln Phe Leu Tyr Lys
 275 280 285
 Trp Thr Val Asn Trp Arg Phe Leu Ser Gln Glu Thr Phe Asn Asn Val
 290 295 300
 His Phe His Gln Leu Leu Phe Ala Leu His Ile Ile Thr Leu Val Leu
 305 310 315 320
 Phe Ile Leu Lys Phe Leu Ser Pro Lys Asn Ile Gly Lys Pro Leu Gly
 325 330 335
 Arg Phe Val Leu Asp Ile Phe Lys Phe Trp Lys Pro Thr Leu Ser Pro
 340 345 350
 Thr Asn Ile Ile Asn Asp Pro Glu Arg Ser Pro Asp Phe Val Tyr Thr
 355 360 365
 Val Met Ala Thr Thr Asn Leu Ile Gly Val Leu Phe Ala Arg Ser Leu
 370 375 380

GFI-108 Sequence listing.ST25

His Tyr Gln Phe Leu Ser Trp Tyr Ala Phe Ser Leu Pro Tyr Leu Leu
385 390 395 400

Tyr Lys Ala Arg Leu Asn Phe Ile Ala Ser Ile Ile Val Tyr Ala Ala
405 410 415

His Glu Tyr Cys Trp Leu Val Phe Pro Ala Thr Glu Gln Ser Ser Ala
420 425 430

Leu Leu Val Ser Ile Leu Leu Leu Ile Leu Ile Leu Ile Phe Thr Asn
435 440 445

Glu Gln Leu Phe Pro Ser Gln Ser Val Pro Ala Glu Lys Lys Asn Thr
450 455 460

<210> 25

<211> 423

<212> PRT

<213> *Pichia pastoris*

<400> 25

Arg Pro Lys Leu Thr Leu Lys Asn Val Ile Gly Asp Leu Val Ala Leu
1 5 10 15

Ile Gln Asn Val Leu Phe Asn Pro Asp Phe Ser Val Phe Val Ala Pro
20 25 30

Leu Leu Trp Leu Ala Asp Ser Ile Val Ile Lys Val Ile Ile Gly Thr
35 40 45

Val Ser Tyr Thr Asp Ile Asp Phe Ser Ser Tyr Met Gln Gln Ile Phe
50 55 60

Lys Ile Arg Gln Gly Glu Leu Asp Tyr Ser Asn Ile Phe Gly Asp Thr
65 70 75 80

Gly Pro Leu Val Tyr Pro Ala Gly His Val His Ala Tyr Ser Val Leu
85 90 95

Ser Trp Tyr Ser Asp Gly Gly Glu Asp Val Ser Phe Val Gln Gln Ala
100 105 110

Phe Gly Trp Leu Tyr Leu Gly Cys Leu Leu Leu Ser Ile Ser Ser Tyr
115 120 125

Phe Phe Ser Gly Leu Gly Lys Ile Pro Pro Val Tyr Phe Val Leu Leu
130 135 140

GFI-108 Sequence listing.ST25

Val Ala Ser Lys Arg Leu His Ser Ile Phe Val Leu Arg Leu Phe Asn
 145 150 155 160

Asp Cys Leu Thr Thr Phe Leu Met Leu Ala Thr Ile Ile Ile Leu Gln
 165 170 175

Gln Ala Ser Ser Trp Arg Lys Asp Gly Thr Thr Ile Pro Leu Ser Val
 180 185 190

Pro Asp Ala Ala Asp Thr Tyr Ser Leu Ala Ile Ser Val Lys Met Asn
 195 200 205

Ala Leu Leu Tyr Leu Pro Ala Phe Leu Leu Leu Ile Tyr Leu Ile Cys
 210 215 220

Asp Glu Asn Leu Ile Lys Ala Leu Ala Pro Val Leu Val Leu Ile Leu
 225 230 235 240

Val Gln Val Gly Val Gly Tyr Ser Phe Ile Leu Pro Leu His Tyr Asp
 245 250 255

Asp Gln Ala Asn Glu Ile Arg Ser Ala Tyr Phe Arg Gln Ala Phe Asp
 260 265 270

Phe Ser Arg Gln Phe Leu Tyr Lys Trp Thr Val Asn Trp Arg Phe Leu
 275 280 285

Ser Gln Glu Thr Phe Asn Asn Val His Phe His Gln Leu Leu Phe Ala
 290 295 300

Leu His Ile Ile Thr Leu Val Leu Phe Ile Leu Lys Phe Leu Ser Pro
 305 310 315 320

Lys Asn Ile Gly Lys Pro Leu Gly Arg Phe Val Leu Asp Ile Phe Lys
 325 330 335

Phe Trp Lys Pro Thr Leu Ser Pro Thr Asn Ile Ile Asn Asp Pro Glu
 340 345 350

Arg Ser Pro Asp Phe Val Tyr Thr Val Met Ala Thr Thr Asn Leu Ile
 355 360 365

Gly Val Leu Phe Ala Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr
 370 375 380

Ala Phe Ser Leu Pro Tyr Leu Leu Tyr Lys Ala Arg Leu Asn Phe Ile
 385 390 395 400

GFI-108 Sequence listing.ST25

Ala Ser Ile Ile Val Tyr Ala Ala His Glu Tyr Cys Trp Leu Val Phe
405 410 415

Pro Ala Thr Glu Gln Ser Ser
420

<210> 26
<211> 398
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 26

Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly Val Arg Tyr
1 5 10 15

Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro Leu Leu Ile
20 25 30

Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys Val Ala Tyr
35 40 45

Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu Met Ile Gln
50 55 60

Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly Thr Gly Pro
65 70 75 80

Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met Met Tyr Trp
85 90 95

Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val Phe Phe Arg
100 105 110

Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys Tyr Tyr Leu
115 120 125

Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu Ser Lys Arg
130 135 140

Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys Phe Thr Thr
145 150 155 160

Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala Ser Arg Cys
165 170 175

His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val Ile Ser Ala
180 185 190

GFI-108 Sequence listing.ST25

Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu Leu Tyr Phe
195 200 205

Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala Asn Val Ile
210 215 220

Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln Val Ala Val
225 230 235 240

Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu His Cys Ala
245 250 255

Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile Asn Trp Gln
260 265 270

Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His Leu Ala Leu
275 280 285

Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val Thr Arg Tyr
290 295 300

Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His Pro Leu Arg
305 310 315 320

Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile Pro Phe Val
325 330 335

Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg Ser Leu His
340 345 350

Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile Leu Ile Phe
355 360 365

Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr Val Leu His
370 375 380

Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala Ser
385 390 395

<210> 27

<211> 398

<212> PRT

<213> Pichia pastoris

<400> 27

Ser Val Phe Val Ala Pro Leu Leu Trp Leu Ala Asp Ser Ile Val Ile
1 5 10 15

GFI-108 Sequence listing.ST25

Lys Val Ile Ile Gly Thr Val Ser Tyr Thr Asp Ile Asp Phe Ser Ser
20 25 30

Tyr Met Gln Gln Ile Phe Lys Ile Arg Gln Gly Glu Leu Asp Tyr Ser
35 40 45

Asn Ile Phe Gly Asp Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val
50 55 60

His Ala Tyr Ser Val Leu Ser Trp Tyr Ser Asp Gly Gly Glu Asp Val
65 70 75 80

Ser Phe Val Gln Gln Ala Phe Gly Trp Leu Tyr Leu Gly Cys Leu Leu
85 90 95

Leu Ser Ile Ser Ser Tyr Phe Phe Ser Gly Leu Gly Lys Ile Pro Pro
100 105 110

Val Tyr Phe Val Leu Leu Val Ala Ser Lys Arg Leu His Ser Ile Phe
115 120 125

Val Leu Arg Leu Phe Asn Asp Cys Leu Thr Thr Phe Leu Met Leu Ala
130 135 140

Thr Ile Ile Ile Leu Gln Gln Ala Ser Ser Trp Arg Lys Asp Gly Thr
145 150 155 160

Thr Ile Pro Leu Ser Val Pro Asp Ala Ala Asp Thr Tyr Ser Leu Ala
165 170 175

Ile Ser Val Lys Met Asn Ala Leu Leu Tyr Leu Pro Ala Phe Leu Leu
180 185 190

Leu Ile Tyr Leu Ile Cys Asp Glu Asn Leu Ile Lys Ala Leu Ala Pro
195 200 205

Val Leu Val Leu Ile Leu Val Gln Val Gly Val Gly Tyr Ser Phe Ile
210 215 220

Leu Pro Leu His Tyr Asp Asp Gln Ala Asn Glu Ile Arg Ser Ala Tyr
225 230 235 240

Phe Arg Gln Ala Phe Asp Phe Ser Arg Gln Phe Leu Tyr Lys Trp Thr
245 250 255

Val Asn Trp Arg Phe Leu Ser Gln Glu Thr Phe Asn Asn Val His Phe
260 265 270

GFI-108 Sequence listing.ST25

His Gln Leu Leu Phe Ala Leu His Ile Ile Thr Leu Val Leu Phe Ile
275 280 285

Leu Lys Phe Leu Ser Pro Lys Asn Ile Gly Lys Pro Leu Gly Arg Phe
290 295 300

Val Leu Asp Ile Phe Lys Phe Trp Lys Pro Thr Leu Ser Pro Thr Asn
305 310 315 320

Ile Ile Asn Asp Pro Glu Arg Ser Pro Asp Phe Val Tyr Thr Val Met
325 330 335

Ala Thr Thr Asn Leu Ile Gly Val Leu Phe Ala Arg Ser Leu His Tyr
340 345 350

Gln Phe Leu Ser Trp Tyr Ala Phe Ser Leu Pro Tyr Leu Leu Tyr Lys
355 360 365

Ala Arg Leu Asn Phe Ile Ala Ser Ile Ile Val Tyr Ala Ala His Glu
370 375 380

Tyr Cys Trp Leu Val Phe Pro Ala Thr Glu Gln Ser Ser Ala
385 390 395

<210> 28

<211> 373

<212> PRT

<213> Neurospora crassa

<400> 28

Ser Lys Leu Ile Pro Pro Ala Leu Phe Leu Val Asp Ala Leu Leu Cys
1 5 10 15

Gly Leu Ile Ile Trp Lys Val Pro Tyr Thr Glu Ile Asp Trp Ala Ala
20 25 30

Tyr Met Glu Gln Val Ser Gln Ile Leu Ser Gly Glu Arg Asp Tyr Thr
35 40 45

Lys Val Arg Gly Gly Thr Gly Pro Leu Val Tyr Pro Ala Ala His Val
50 55 60

Tyr Ile Tyr Thr Gly Leu Tyr His Leu Thr Asp Glu Gly Arg Asn Ile
65 70 75 80

Leu Leu Ala Gln Gln Leu Phe Ala Gly Leu Tyr Met Val Thr Leu Ala
85 90 95

GFI-108 Sequence listing.ST25

val val Met Gly Cys Tyr Trp Gln Ala Lys Ala Pro Pro Tyr Leu Phe
100 105 110

Pro Leu Leu Thr Leu Ser Lys Arg Leu His Ser Ile Phe Val Leu Arg
115 120 125

Cys Phe Asn Asp Cys Phe Ala Val Leu Phe Leu Trp Leu Ala Ile Phe
130 135 140

Phe Phe Gln Arg Arg Asn Trp Gln Ala Gly Ala Leu Leu Tyr Thr Leu
145 150 155 160

Gly Leu Gly Val Lys Met Thr Leu Leu Ser Leu Pro Ala Val Gly
165 170 175

Ile Val Leu Phe Leu Gly Ser Gly Ser Phe Val Thr Thr Leu Gln Leu
180 185 190

Val Ala Thr Met Gly Leu Val Gln Ile Leu Ile Gly Val Pro Phe Leu
195 200 205

Ala His Tyr Pro Thr Glu Tyr Leu Ser Arg Ala Phe Glu Leu Ser Arg
210 215 220

Gln Phe Phe Phe Lys Trp Thr Val Asn Trp Arg Phe Val Gly Glu Glu
225 230 235 240

Ile Phe Leu Ser Lys Gly Phe Ala Leu Thr Leu Leu Ala Leu His Val
245 250 255

Leu Val Leu Gly Ile Phe Ile Thr Thr Arg Trp Ile Lys Pro Ala Arg
260 265 270

Lys Ser Leu Val Gln Leu Ile Ser Pro Val Leu Leu Ala Gly Lys Pro
275 280 285

Pro Leu Thr Val Pro Glu His Arg Ala Ala Ala Arg Asp Val Thr Pro
290 295 300

Arg Tyr Ile Met Thr Thr Ile Leu Ser Ala Asn Ala Val Gly Leu Leu
305 310 315 320

Phe Ala Arg Ser Leu His Tyr Gln Phe Tyr Ala Tyr Val Ala Trp Ser
325 330 335

Thr Pro Phe Leu Leu Trp Arg Ala Gly Leu His Pro Val Leu Val Tyr
Page 28

GFI-108 Sequence listing.ST25
340 345 350

Leu Leu Trp Ala Val His Glu Trp Ala Trp Asn Val Phe Pro Ser Thr
355 360 365

Pro Ala Ser Ser Ala
370

<210> 29
<211> 390
<212> PRT
<213> Pichia pastoris

<400> 29

Leu Trp Leu Ala Asp Ser Ile Val Ile Lys Val Ile Ile Gly Thr Val
1 5 10 15

Ser Tyr Thr Asp Ile Asp Phe Ser Ser Tyr Met Gln Gln Ile Phe Lys
20 25 30

Ile Arg Gln Gly Glu Leu Asp Tyr Ser Asn Ile Phe Gly Asp Thr Gly
35 40 45

Pro Leu Val Tyr Pro Ala Gly His Val His Ala Tyr Ser Val Leu Ser
50 55 60

Trp Tyr Ser Asp Gly Gly Glu Asp Val Ser Phe Val Gln Gln Ala Phe
65 70 75 80

Gly Trp Leu Tyr Leu Gly Cys Leu Leu Leu Ser Ile Ser Ser Tyr Phe
85 90 95

Phe Ser Gly Leu Gly Lys Ile Pro Pro Val Tyr Phe Val Leu Leu Val
100 105 110

Ala Ser Lys Arg Leu His Ser Ile Phe Val Leu Arg Leu Phe Asn Asp
115 120 125

Cys Leu Thr Thr Phe Leu Met Leu Ala Thr Ile Ile Ile Leu Gln Gln
130 135 140

Ala Ser Ser Trp Arg Lys Asp Gly Thr Thr Ile Pro Leu Ser Val Pro
145 150 155 160

Asp Ala Ala Asp Thr Tyr Ser Leu Ala Ile Ser Val Lys Met Asn Ala
165 170 175

Leu Leu Tyr Leu Pro Ala Phe Leu Leu Ile Tyr Leu Ile Cys Asp
Page 29

GFI-108 Sequence listing.ST25

180

185

190

Glu Asn Leu Ile Lys Ala Leu Ala Pro Val Leu Val Leu Ile Leu Val
 195 200 205

Gln Val Gly Val Gly Tyr Ser Phe Ile Leu Pro Leu His Tyr Asp Asp
 210 215 220

Gln Ala Asn Glu Ile Arg Ser Ala Tyr Phe Arg Gln Ala Phe Asp Phe
 225 230 235 240

Ser Arg Gln Phe Leu Tyr Lys Trp Thr Val Asn Trp Arg Phe Leu Ser
 245 250 255

Gln Glu Thr Phe Asn Asn Val His Phe His Gln Leu Leu Phe Ala Leu
 260 265 270

His Ile Ile Thr Leu Val Leu Phe Ile Leu Lys Phe Leu Ser Pro Lys
 275 280 285

Asn Ile Gly Lys Pro Leu Gly Arg Phe Val Leu Asp Ile Phe Lys Phe
 290 295 300

Trp Lys Pro Thr Leu Ser Pro Thr Asn Ile Ile Asn Asp Pro Glu Arg
 305 310 315 320

Ser Pro Asp Phe Val Tyr Thr Val Met Ala Thr Thr Asn Leu Ile Gly
 325 330 335

Val Leu Phe Ala Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr Ala
 340 345 350

Phe Ser Leu Pro Tyr Leu Leu Tyr Lys Ala Arg Leu Asn Phe Ile Ala
 355 360 365

Ser Ile Ile Val Tyr Ala Ala His Glu Tyr Cys Trp Leu Val Phe Pro
 370 375 380

Ala Thr Glu Gln Ser Ser
 385 390

<210> 30

<211> 355

<212> PRT

<213> Schizosaccharomyces pombe

<400> 30

Leu Leu Leu Glu Ile Pro Phe Val Phe Ala Ile Ile Ser Lys Val

GFI-108 Sequence listing.ST25

1

5

10

15

Pro Tyr Thr Glu Ile Asp Trp Ile Ala Tyr Met Glu Gln Val Asn Ser
20 25 30

Phe Leu Leu Gly Glu Arg Asp Tyr Lys Ser Leu Val Gly Cys Thr Gly
35 40 45

Pro Leu Val Tyr Pro Gly Gly His Val Phe Leu Tyr Thr Leu Leu Tyr
50 55 60

Tyr Leu Thr Asp Gly Gly Thr Asn Ile Val Arg Ala Gln Tyr Ile Phe
65 70 75 80

Ala Phe Val Tyr Trp Ile Thr Thr Ala Ile Val Gly Tyr Leu Phe Lys
85 90 95

Ile Val Arg Ala Pro Phe Tyr Ile Tyr Val Leu Leu Ile Leu Ser Lys
100 105 110

Arg Leu His Ser Ile Phe Ile Leu Arg Leu Phe Asn Asp Gly Phe Asn
115 120 125

Ser Leu Phe Ser Ser Leu Phe Ile Leu Ser Ser Cys Lys Lys Lys Trp
130 135 140

Val Arg Ala Ser Ile Leu Leu Ser Val Ala Cys Ser Val Lys Met Ser
145 150 155 160

Ser Leu Leu Tyr Val Pro Ala Tyr Leu Val Leu Leu Leu Gln Ile Leu
165 170 175

Gly Pro Lys Lys Thr Trp Met His Ile Phe Val Ile Ile Ile Val Gln
180 185 190

Ile Leu Phe Ser Ile Pro Phe Leu Ala Tyr Phe Trp Ser Tyr Trp Thr
195 200 205

Gln Ala Phe Asp Phe Gly Arg Ala Phe Asp Tyr Lys Trp Thr Val Asn
210 215 220

Trp Arg Phe Ile Pro Arg Ser Ile Phe Glu Ser Thr Ser Phe Ser Thr
225 230 235 240

Ser Ile Leu Phe Leu His Val Ala Leu Leu Val Ala Phe Thr Cys Lys
245 250 255

GFI-108 Sequence listing. ST25

His Trp Asn Lys Leu Ser Arg Ala Thr Pro Phe Ala Met Val Asn Ser
260 265 270

Met Leu Thr Leu Lys Pro Leu Pro Lys Leu Gln Leu Ala Thr Pro Asn
275 280 285

Phe Ile Phe Thr Ala Leu Ala Thr Ser Asn Leu Ile Gly Ile Leu Cys
290 295 300

Ala Arg Ser Leu His Tyr Gln Phe Tyr Ala Trp Phe Ala Trp Tyr Ser
305 310 315 320

Pro Tyr Leu Cys Tyr Gln Ala Ser Phe Pro Ala Pro Ile Val Ile Gly
325 330 335

Leu Trp Met Leu Gln Glu Tyr Ala Trp Asn Val Phe Pro Ser Thr Lys
340 345 350

Leu Ser Ser
355

<210> 31
<211> 390
<212> PRT
<213> *Pichia pastoris*

<400> 31

Leu Trp Leu Ala Asp Ser Ile Val Ile Lys Val Ile Ile Gly Thr Val
1 5 10 15

Ser Tyr Thr Asp Ile Asp Phe Ser Ser Tyr Met Gln Gln Ile Phe Lys
20 25 30

Ile Arg Gln Gly Glu Leu Asp Tyr Ser Asn Ile Phe Gly Asp Thr Gly
35 40 45

Pro Leu Val Tyr Pro Ala Gly His Val His Ala Tyr Ser Val Leu Ser
50 55 60

Trp Tyr Ser Asp Gly Gly Glu Asp Val Ser Phe Val Gln Gln Ala Phe
65 70 75 80

Gly Trp Leu Tyr Leu Gly Cys Leu Leu Ser Ile Ser Ser Tyr Phe
85 90 95

Phe Ser Gly Leu Gly Lys Ile Pro Pro Val Tyr Phe Val Leu Leu Val
100 105 110

GFI-108 Sequence listing.ST25

Ala Ser Lys Arg Leu His Ser Ile Phe Val Leu Arg Leu Phe Asn Asp
 115 120 125

Cys Leu Thr Thr Phe Leu Met Leu Ala Thr Ile Ile Ile Leu Gln Gln
 130 135 140

Ala Ser Ser Trp Arg Lys Asp Gly Thr Thr Ile Pro Leu Ser Val Pro
 145 150 155 160

Asp Ala Ala Asp Thr Tyr Ser Leu Ala Ile Ser Val Lys Met Asn Ala
 165 170 175

Leu Leu Tyr Leu Pro Ala Phe Leu Leu Leu Ile Tyr Leu Ile Cys Asp
 180 185 190

Glu Asn Leu Ile Lys Ala Leu Ala Pro Val Leu Val Leu Ile Leu Val
 195 200 205

Gln Val Gly Val Gly Tyr Ser Phe Ile Leu Pro Leu His Tyr Asp Asp
 210 215 220

Gln Ala Asn Glu Ile Arg Ser Ala Tyr Phe Arg Gln Ala Phe Asp Phe
 225 230 235 240

Ser Arg Gln Phe Leu Tyr Lys Trp Thr Val Asn Trp Arg Phe Leu Ser
 245 250 255

Gln Glu Thr Phe Asn Asn Val His Phe His Gln Leu Leu Phe Ala Leu
 260 265 270

His Ile Ile Thr Leu Val Leu Phe Ile Leu Lys Phe Leu Ser Pro Lys
 275 280 285

Asn Ile Gly Lys Pro Leu Gly Arg Phe Val Leu Asp Ile Phe Lys Phe
 290 295 300

Trp Lys Pro Thr Leu Ser Pro Thr Asn Ile Ile Asn Asp Pro Glu Arg
 305 310 315 320

Ser Pro Asp Phe Val Tyr Thr Val Met Ala Thr Thr Asn Leu Ile Gly
 325 330 335

Val Leu Phe Ala Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr Ala
 340 345 350

Phe Ser Leu Pro Tyr Leu Leu Tyr Lys Ala Arg Leu Asn Phe Ile Ala
 355 360 365

GFI-108 Sequence listing.ST25

Ser Ile Ile Val Tyr Ala Ala His Glu Tyr Cys Trp Leu Val Phe Pro
370 375 380

Ala Thr Glu Gln Ser Ser
385 390

<210> 32
<211> 363
<212> PRT
<213> *Arabidopsis thaliana*

<400> 32

Leu Ile Leu Ala Asp Ala Ile Leu Val Ala Leu Ile Ile Ala Tyr Val
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Pro Tyr Thr Lys Ile Asp Trp Asp Ala Tyr Met Ser Gln Val Ser Gly
20 25 30

Phe Leu Gly Gly Glu Arg Asp Tyr Gly Asn Leu Lys Gly Asp Thr Gly
35 40 45

Pro Leu Val Tyr Pro Ala Gly Phe Leu Tyr Val Tyr Ser Ala Val Gln
50 55 60

Asn Leu Thr Gly Gly Glu Val Tyr Pro Ala Gln Ile Leu Phe Gly Val
65 70 75 80

Leu Tyr Ile Val Asn Leu Gly Ile Val Leu Ile Ile Tyr Val Lys Thr
85 90 95

Asp Val Val Pro Trp Trp Ala Leu Ser Leu Leu Cys Leu Ser Lys Arg
100 105 110

Ile His Ser Ile Phe Val Leu Arg Leu Phe Asn Asp Cys Phe Ala Met
115 120 125

Thr Leu Leu His Ala Ser Met Ala Leu Phe Leu Tyr Arg Lys Trp His
130 135 140

Leu Gly Met Leu Val Phe Ser Gly Ala Val Ser Val Lys Met Asn Val
145 150 155 160

Leu Leu Tyr Ala Pro Thr Leu Leu Leu Leu Leu Lys Ala Met Asn
165 170 175

Ile Ile Gly Val Val Ser Ala Leu Ala Gly Ala Ala Leu Ala Gln Ile
180 185 190

GFI-108 Sequence listing.ST25

Leu Val Gly Leu Pro Phe Leu Ile Thr Tyr Pro Val Ser Tyr Ile Ala
195 200 205

Asn Ala Phe Asp Leu Gly Arg Val Phe Ile His Phe Trp Ser Val Asn
210 215 220

Phe Lys Phe Val Pro Glu Arg Val Phe Val Ser Lys Glu Phe Ala Val
225 230 235 240

Cys Leu Leu Ile Ala His Leu Phe Leu Leu Val Ala Phe Ala Asn Tyr
245 250 255

Lys Trp Cys Lys His Glu Gly Gly Ile Ile Gly Phe Met Arg Ser Arg
260 265 270

His Phe Phe Leu Thr Leu Pro Ser Ser Leu Ser Phe Ser Asp Val Ser
275 280 285

Ala Ser Arg Ile Ile Thr Lys Glu His Val Val Thr Ala Met Phe Val
290 295 300

Gly Asn Phe Ile Gly Ile Val Phe Ala Arg Ser Leu His Tyr Gln Phe
305 310 315 320

Tyr Ser Trp Tyr Phe Tyr Ser Leu Pro Tyr Leu Leu Trp Arg Thr Pro
325 330 335

Phe Pro Thr Trp Leu Arg Leu Ile Met Phe Leu Gly Ile Glu Leu Cys
340 345 350

Trp Asn Val Tyr Pro Ser Thr Pro Ser Ser Ser
355 360

<210> 33
<211> 428
<212> DNA
<213> *Kluyveromyces lactis*

<400> 33		
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gaacaaattg catacatttt acttgttacc aattacattg gagtactatt tgctcgatca	180	
ttacactacc aattcctatc ttggtaccat tggacgttac cagtactatt gaattgggcc	240	
aatgttccgt atccgctatg tgtgctatgg tacctaacac atgagtggtg ctggaacagc	300	
tatccgccaa acgctactgc atccacactg ctacacgcgt gtaacacata ctgttattgg	360	

GFI-108 Sequence listing.ST25

ctgtattctt aagaggaccc gcaaactcgaa 420
aagctgag 428

<210> 34

<211> 142

<212> PRT

<213> Kluyveromyces lactis

<400> 34

Phe Val Tyr Lys Leu Ile Pro Thr Asn Met Asn Thr Pro Ala Gly Leu
1 5 10 15

Leu Lys Ile Gly Lys Ala Asn Leu Leu His Pro Phe Thr Asp Ala Val
20 25 30

Phe Ser Ala Met Arg Val Asn Ala Glu Gln Ile Ala Tyr Ile Leu Leu
35 40 45

Val Thr Asn Tyr Ile Gly Val Leu Phe Ala Arg Ser Leu His Tyr Gln
50 55 60

Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Val Leu Leu Asn Trp Ala
65 70 75 80

Asn Val Pro Tyr Pro Leu Cys Val Leu Trp Tyr Leu Thr His Glu Trp
85 90 95

Cys Trp Asn Ser Tyr Pro Pro Asn Ala Thr Ala Ser Thr Leu Leu His
100 105 110

Ala Cys Asn Thr Tyr Cys Tyr Trp Leu Tyr Ser Glx Glu Asp Pro Gln
115 120 125

Thr Arg Lys Val Val Ile Thr Lys Gln His Thr Arg Lys Leu
130 135 140

<210> 35

<211> 102

<212> PRT

<213> Kluyveromyces lactis

<400> 35

Ala Asn Leu Leu His Pro Phe Thr Asp Ala Val Phe Ser Ala Met Arg
1 5 10 15

Val Asn Ala Glu Gln Ile Ala Tyr Ile Leu Leu Val Thr Asn Tyr Ile
20 25 30

GFI-108 Sequence listing.ST25

Gly Val Leu Phe Ala Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr
35 40 45

His Trp Thr Leu Pro Val Leu Leu Asn Trp Ala Asn Val Pro Tyr Pro
50 55 60

Leu Cys Val Leu Trp Tyr Leu Thr His Glu Trp Cys Trp Asn Ser Tyr
65 70 75 80

Pro Pro Asn Ala Thr Ala Ser Thr Leu Leu His Ala Cys Asn Thr Tyr
85 90 95

Cys Tyr Trp Leu Tyr Ser
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<210> 36

<211> 16

<212> PRT

<213> Kluyveromyces lactis

<400> 36

Glu Asp Pro Gln Thr Arg Lys Val Val Ile Thr Lys Gln His Thr Arg
1 5 10 15

<210> 37

<211> 117

<212> PRT

<213> Saccharomyces cerevisiae

<400> 37

Ser Ser Leu Cys His Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn
1 5 10 15

Pro Ala Lys Thr Ile Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly
20 25 30

Val Leu Phe Ser Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His
35 40 45

Trp Thr Leu Pro Ile Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val
50 55 60

Gly Pro Ile Trp Tyr Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro
65 70 75 80

Pro Asn Ser Gln Ala Ser Thr Leu Leu Ala Leu Asn Thr Val Leu
85 90 95

Leu Leu Leu Ala Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala
Page 37

Lys Ser His Leu Arg
115

<210> 38
<211> 96
<212> PRT
<213> *Kluyveromyces lactis*

<400> 38

Phe Thr Asp Ala Val Phe Ser Ala Met Arg Val Asn Ala Glu Gln Ile
1 5 10 15

Ala Tyr Ile Leu Leu Val Thr Asn Tyr Ile Gly Val Leu Phe Ala Arg
20 25 30

Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Val
35 40 45

Leu Leu Asn Trp Ala Asn Val Pro Tyr Pro Leu Cys Val Leu Trp Tyr
50 55 60

Leu Thr His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ala Thr Ala
65 70 75 80

Ser Thr Leu Leu His Ala Cys Asn Thr Tyr Cys Tyr Trp Leu Tyr Ser
85 90 95

<210> 39
<211> 7
<212> PRT
<213> *Kluyveromyces lactis*

<400> 39

Glu Asp Pro Gln Thr Arg Lys
1 5

<210> 40
<211> 106
<212> PRT
<213> *Arabidopsis thaliana*

<400> 40

Phe Ser Asp Val Ser Ala Ser Arg Ile Ile Thr Lys Glu His Val Val
1 5 10 15

Thr Ala Met Phe Val Gly Asn Phe Ile Gly Ile Val Phe Ala Arg Ser
20 25 30

GFI-108 Sequence listing.ST25

Leu His Tyr Gln Phe Tyr Ser Trp Tyr Phe Tyr Ser Leu Pro Tyr Leu
35 40 45

Leu Trp Arg Thr Pro Phe Pro Thr Trp Leu Arg Leu Ile Met Phe Leu
50 55 60

Gly Ile Glu Leu Cys Trp Asn Val Tyr Pro Ser Thr Pro Ser Ser Ser
65 70 75 80

Gly Leu Leu Leu Cys Leu His Leu Ile Ile Leu Val Gly Leu Trp Leu
85 90 95

Ala Pro Ser Val Asp Pro Tyr Gln Leu Lys
100 105

<210> 41
<211> 4
<212> PRT
<213> artificial

<220>
<223> Signal tetrapeptide

<400> 41

His Asp Glu Leu
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<210> 42
<211> 4
<212> PRT
<213> artificial

<220>
<223> Signal tetrapeptide

<400> 42

Lys Asp Glu Leu
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<210> 43
<400> 43
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<210> 44
<400> 44
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<210> 45
<211> 1617
<212> DNA
<213> Mus musculus

GFI-108 Sequence listing.ST25

<400> 45	
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ctcagcccta acctcgatc cagcttcttc tggacaatg cccctgtcac tccccaggcc	180
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ctccagccac tgtccccgag caaggccaca gaggaactgc accgggtgga cttcgtgttgc	300
ccggaggaca ccacggagta ttttgtgcgc accaaagctg gtggtgtgtg cttcaaaccac	360
ggtaccagga tgctggagaa accttcgcca gggcggacag aggagaagcc cgaagtgtct	420
gagggctcct cagcccgaaa acctgctcg aggccatga ggcacgtgtt gagtacgcgg	480
gagcgcctgg gcagccgggg cactaggcgc aagtgggttgc agtgtgtgtg cctgccaggc	540
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gaacgcctgg tacccagggaa ggtaccgagg cgggttatca acgccatcaa catcaaccac	660
gagttcgacc tgctggatgt gcgcttccat gagctggag atgttgtgga cgccttcgtg	720
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acccaggatg gcgtctcccg cctgcgcaac ctgcggcccg atgacgtctt tatcatcgac	960
gatgcggacg agatccctgc gcgtgatggt gtgctgttcc tcaaactcta cgatggctgg	1020
acagagccct tcgccttcca catgcggaag tccctgtatg gtttcttctg gaagcagccg	1080
ggcacactgg aggtgggtgc aggctgcacc atggacatgc tgcaggccgt gtatggctg	1140
gatggcatcc gcctgcgccc cgcgcgtac tacaccatgc ccaacttcgc gcagtatgag	1200
aaccgcaccgc gccacatcct agtgcagtgg tctctcgca gccccctgc cttcgccggc	1260
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ttgctggaaa atccctaccg ggagcccaag agcactgttag aggggtggcgc ccagaaccag	1560
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<210> 46	
<211> 536	
<212> PRT	
<213> <i>Mus musculus</i>	

<400> 46

GFI-108 Sequence listing.ST25

Met Arg Arg Tyr Lys Leu Phe Leu Met Phe Cys Met Ala Gly Leu Cys
1 5 10 15

Leu Ile Ser Phe Leu His Phe Phe Lys Thr Leu Ser Tyr Val Thr Phe
20 25 30

Pro Arg Glu Leu Ala Ser Leu Ser Pro Asn Leu Ile Ser Ser Phe Phe
35 40 45

Trp Asn Asn Ala Pro Val Thr Pro Gln Ala Ser Pro Glu Pro Gly Asp
50 55 60

Pro Asp Leu Leu Arg Thr Pro Leu Tyr Ser His Ser Pro Leu Leu Gln
65 70 75 80

Pro Leu Ser Pro Ser Lys Ala Thr Glu Glu Leu His Arg Val Asp Phe
85 90 95

Val Leu Pro Glu Asp Thr Thr Glu Tyr Phe Val Arg Thr Lys Ala Gly
100 105 110

Gly Val Cys Phe Lys Pro Gly Thr Arg Met Leu Glu Lys Pro Ser Pro
115 120 125

Gly Arg Thr Glu Glu Lys Thr Glu Val Ser Glu Gly Ser Ser Ala Arg
130 135 140

Gly Pro Ala Arg Arg Pro Met Arg His Val Leu Ser Ser Arg Glu Arg
145 150 155 160

Leu Gly Ser Arg Gly Thr Arg Arg Lys Trp Val Glu Cys Val Cys Leu
165 170 175

Pro Gly Trp His Gly Pro Ser Cys Gly Val Pro Thr Val Val Gln Tyr
180 185 190

Ser Asn Leu Pro Thr Lys Glu Arg Leu Val Pro Arg Glu Val Pro Arg
195 200 205

Arg Val Ile Asn Ala Ile Asn Ile Asn His Glu Phe Asp Leu Leu Asp
210 215 220

Val Arg Phe His Glu Leu Gly Asp Val Val Asp Ala Phe Val Val Cys
225 230 235 240

Asp Ser Asn Phe Thr Ala Tyr Gly Glu Pro Arg Pro Leu Lys Phe Arg
245 250 255

GFI-108 Sequence listing.ST25

Glu Met Leu Thr Asn Gly Thr Phe Glu Tyr Ile Arg His Lys Val Leu
260 265 270

Tyr Val Phe Leu Asp His Phe Pro Pro Gly Gly Arg Gln Asp Gly Trp
275 280 285

Ile Ala Asp Asp Tyr Leu Arg Thr Phe Leu Thr Gln Asp Gly Val Ser
290 295 300

Arg Leu Arg Asn Leu Arg Pro Asp Asp Val Phe Ile Ile Asp Asp Ala
305 310 315 320

Asp Glu Ile Pro Ala Arg Asp Gly Val Leu Phe Leu Lys Leu Tyr Asp
325 330 335

Gly Trp Thr Glu Pro Phe Ala Phe His Met Arg Lys Ser Leu Tyr Gly
340 345 350

Phe Phe Trp Lys Gln Pro Gly Thr Leu Glu Val Val Ser Gly Cys Thr
355 360 365

Met Asp Met Leu Gln Ala Val Tyr Gly Leu Asp Gly Ile Arg Leu Arg
370 375 380

Arg Arg Gln Tyr Tyr Thr Met Pro Asn Phe Arg Gln Tyr Glu Asn Arg
385 390 395 400

Thr Gly His Ile Leu Val Gln Trp Ser Leu Gly Ser Pro Leu His Phe
405 410 415

Ala Gly Trp His Cys Ser Trp Cys Phe Thr Pro Glu Gly Ile Tyr Phe
420 425 430

Lys Leu Val Ser Ala Gln Asn Gly Asp Phe Pro Arg Trp Gly Asp Tyr
435 440 445

Glu Asp Lys Arg Asp Leu Asn Tyr Ile Arg Ser Leu Ile Arg Thr Gly
450 455 460

Gly Trp Phe Asp Gly Thr Gln Gln Glu Tyr Pro Pro Ala Asp Pro Ser
465 470 475 480

Glu His Met Tyr Ala Pro Lys Tyr Leu Leu Lys Asn Tyr Asp Gln Phe
485 490 495

Arg Tyr Leu Leu Glu Asn Pro Tyr Arg Glu Pro Lys Ser Thr Val Glu

GFI-108 Sequence listing.ST25
 500 505 510

Gly Gly Arg Gln Asn Gln Gly Ser Asp Gly Arg Ser Ser Ala Val Arg
 515 520 525

Gly Lys Leu Asp Thr Ala Glu Gly
 530 535

<210> 47
 <211> 21
 <212> DNA
 <213> artificial

<220>
 <223> cloning primer

<400> 47
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21

<210> 48
 <211> 22
 <212> DNA
 <213> artificial

<220>
 <223> cloning primer

<400> 48
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22

<210> 49
 <211> 20
 <212> DNA
 <213> artificial

<220>
 <223> cloning primer

<400> 49
 atttaaccct cactaaaggg

20

<210> 50
 <211> 1968
 <212> DNA
 <213> Mus musculus

<400> 50
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 accgagaagt tcgtgctgct gctgggtttc agcgcccttca tcacgctctg cttcggggca 180
 atcttcttcc tgcctgactc ctccaaagctg ctcagcgggg tcctgttcca ctccaaaccct 240
 gccttgcagc cgccggcggga gcacaagccc gggctcgggg cgctgcggga ggatgccgccc 300

GFI-108 Sequence listing. ST25

gaggggagag tccggcaccg cgaggaaggc ggcgcctgggg accctggagc tggactggaa	360
gacaacttag ccaggatccg cgaaaaccac gagcgggctc tcagggaaagc caaggagacc	420
ctgcagaagc tgccggagga gatccaaaga gacattctgc tggagaagga aaaggtggcc	480
caggaccagc tgcgtgacaa ggatctgtt aggggcttgc ccaaggtgga cttcctgccc	540
cccgctgggg tagagaaccc ggagcccgct gacgccacca tccgtgagaa gagggcaaag	600
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gaactgaaac ctatataaaa agaaggccat tcaagcagtt tgtttggcaa catcaaagga	720
gctacaatag tagatgcctt ggataccctt ttcattatgg gcatgaagac tgaatttcaa	780
gaagctaaat cgtggattaa aaaatattta gattttaaatg tgaatgctga agtttctgtt	840
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ccctctggaa taccttgggc attgctgaat atgaaaagtgg gatcgcccg gaactggccc	1020
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gaactcggag ctgaaattgc ccgcacttgt catgaatctt ataatcgtac atatgtgaag	1560
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gaaaagtatt acatcttacg gcccgggtc atcgagacat acatgtacat gtggcgactg	1680
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gacgatgtcc agcaaagttt cttcctggca gagacactga agtatttgc tttgatattt	1860
tccgatgtatg accttcttcc actagaacac tggatcttca acaccgaggc tcattccttc	1920
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<210> 51
<211> 655
<212> PRT
<213> *Mus musculus*

<400> 51

GFI-108 Sequence listing.ST25

Met Pro Val Gly Gly Leu Leu Pro Leu Phe Ser Ser Pro Gly Gly Gly
1 5 10 15

Gly Leu Gly Ser Gly Leu Gly Gly Leu Gly Gly Gly Arg Lys Gly
20 25 30

Ser Gly Pro Ala Ala Phe Arg Leu Thr Glu Lys Phe Val Leu Leu Leu
35 40 45

Val Phe Ser Ala Phe Ile Thr Leu Cys Phe Gly Ala Ile Phe Phe Leu
50 55 60

Pro Asp Ser Ser Lys Leu Leu Ser Gly Val Leu Phe His Ser Asn Pro
65 70 75 80

Ala Leu Gln Pro Pro Ala Glu His Lys Pro Gly Leu Gly Ala Arg Ala
85 90 95

Glu Asp Ala Ala Glu Gly Arg Val Arg His Arg Glu Glu Gly Ala Pro
100 105 110

Gly Asp Pro Gly Ala Gly Leu Glu Asp Asn Leu Ala Arg Ile Arg Glu
115 120 125

Asn His Glu Arg Ala Leu Arg Glu Ala Lys Glu Thr Leu Gln Lys Leu
130 135 140

Pro Glu Glu Ile Gln Arg Asp Ile Leu Leu Glu Lys Glu Lys Val Ala
145 150 155 160

Gln Asp Gln Leu Arg Asp Lys Asp Leu Phe Arg Gly Leu Pro Lys Val
165 170 175

Asp Phe Leu Pro Pro Val Gly Val Glu Asn Arg Glu Pro Ala Asp Ala
180 185 190

Thr Ile Arg Glu Lys Arg Ala Lys Ile Lys Glu Met Met Thr His Ala
195 200 205

Trp Asn Asn Tyr Lys Arg Tyr Ala Trp Gly Leu Asn Glu Leu Lys Pro
210 215 220

Ile Ser Lys Glu Gly His Ser Ser Ser Leu Phe Gly Asn Ile Lys Gly
225 230 235 240

Ala Thr Ile Val Asp Ala Leu Asp Thr Leu Phe Ile Met Gly Met Lys
245 250 255

GFI-108 Sequence listing.ST25

Thr Glu Phe Gln Glu Ala Lys Ser Trp Ile Lys Lys Tyr Leu Asp Phe
260 265 270

Asn Val Asn Ala Glu Val Ser Val Phe Glu Val Asn Ile Arg Phe Val
275 280 285

Gly Gly Leu Leu Ser Ala Tyr Tyr Leu Ser Gly Glu Glu Ile Phe Arg
290 295 300

Lys Lys Ala Val Glu Leu Gly Val Lys Leu Leu Pro Ala Phe His Thr
305 310 315 320

Pro Ser Gly Ile Pro Trp Ala Leu Leu Asn Met Lys Ser Gly Ile Gly
325 330 335

Arg Asn Trp Pro Trp Ala Ser Gly Gly Ser Ser Ile Leu Ala Glu Phe
340 345 350

Gly Thr Leu His Leu Glu Phe Met His Leu Ser His Leu Ser Gly Asp
355 360 365

Pro Val Phe Ala Glu Lys Val Met Lys Ile Arg Thr Val Leu Asn Lys
370 375 380

Leu Asp Lys Pro Glu Gly Leu Tyr Pro Asn Tyr Leu Asn Pro Ser Ser
385 390 395 400

Gly Gln Trp Gly Gln His His Val Ser Val Gly Gly Leu Gly Asp Ser
405 410 415

Phe Tyr Glu Tyr Leu Leu Lys Ala Trp Leu Met Ser Asp Lys Thr Asp
420 425 430

Leu Glu Ala Lys Lys Met Tyr Phe Asp Ala Val Gln Ala Ile Glu Thr
435 440 445

His Leu Ile Arg Lys Ser Ser Gly Gly Leu Thr Tyr Ile Ala Glu Trp
450 455 460

Lys Gly Gly Leu Leu Glu His Lys Met Gly His Leu Thr Cys Phe Ala
465 470 475 480

Gly Gly Met Phe Ala Leu Gly Ala Asp Gly Ala Pro Glu Ala Arg Ala
485 490 495

Gln His Tyr Leu Glu Leu Gly Ala Glu Ile Ala Arg Thr Cys His Glu
Page 46

GFI-108 Sequence listing.ST25
500 505 510

Ser Tyr Asn Arg Thr Tyr Val Lys Leu Gly Pro Glu Ala Phe Arg Phe
515 520 525

Asp Gly Gly Val Glu Ala Ile Ala Thr Arg Gln Asn Glu Lys Tyr Tyr
530 535 540

Ile Leu Arg Pro Glu Val Ile Glu Thr Tyr Met Tyr Met Trp Arg Leu
545 550 555 560

Thr His Asp Pro Lys Tyr Arg Thr Trp Ala Trp Glu Ala Val Glu Ala
565 570 575

Leu Glu Ser His Cys Arg Val Asn Gly Gly Tyr Ser Gly Leu Arg Asp
580 585 590

Val Tyr Ile Ala Arg Glu Ser Tyr Asp Asp Val Gln Gln Ser Phe Phe
595 600 605

Leu Ala Glu Thr Leu Lys Tyr Leu Tyr Leu Ile Phe Ser Asp Asp Asp
610 615 620

Leu Leu Pro Leu Glu His Trp Ile Phe Asn Thr Glu Ala His Pro Phe
625 630 635 640

Pro Ile Leu Arg Glu Gln Lys Lys Glu Ile Asp Gly Lys Glu Lys
645 650 655

<210> 52
<211> 36
<212> DNA
<213> artificial

<220>
<223> cloning primer

<400> 52
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<210> 53
<211> 40
<212> DNA
<213> artificial

<220>
<223> cloning primer

<400> 53
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GFI-108 Sequence listing.ST25

<210> 54
<211> 44
<212> DNA
<213> artificial

<220>
<223> cloning primer

<400> 54
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44

<210> 55
<211> 50
<212> DNA
<213> artificial

<220>
<223> cloning primer

<400> 55
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50

<210> 56
<211> 51
<212> DNA
<213> artificial

<220>
<223> cloning primer

<400> 56
ggcgagctcg gcctacccgg ccaaggctga gatcatttgt ccagttcag a

51

<210> 57
<211> 55
<212> DNA
<213> artificial

<220>
<223> cloning primer

<400> 57
gcccacgtcg acggatccgt ttaaacatcg attggagagg ctgacaccgc tacta

55

<210> 58
<211> 55
<212> DNA
<213> artificial

<220>
<223> cloning primer

<400> 58
cgggatccac tagtatttaa atcatatgtg cgagtgtaca actcttccca catgg

55

<210> 59
<211> 55
<212> DNA

GFI-108 Sequence listing.ST25

<213> artificial

<220>

<223> cloning primer

<400> 59

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55

<210> 60

<211> 45

<212> DNA

<213> artificial

<220>

<223> cloning primer

<400> 60

cgggatccct cgagagatct ttttgtaga aatgtcttgg tgcct

45

<210> 61

<211> 63

<212> DNA

<213> artificial

<220>

<223> cloning primer

<400> 61

ggacatgcat gcactagtgc ggccgccacg tgatagttgt tcaattgatt gaaataggg

60

caa

63

<210> 62

<211> 52

<212> DNA

<213> artificial

<220>

<223> cloning primer

<400> 62

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52

<210> 63

<211> 61

<212> DNA

<213> artificial

<220>

<223> cloning primer

<400> 63

ggacatgcat gcggatccct taagagccgg cagcttgcaa attaaaggct tcgagcgtcc

60

c

61

<210> 64

<211> 61

GFI-108 Sequence listing.ST25

<212> DNA
<213> artificial

<220>
<223> cloning primer

<400> 64
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c 61

<210> 65
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<210> 66
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<400> 66
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<210> 67
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<220>
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<400> 67
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GFI-108 Sequence listing.ST25

<213> artificial

<220>

<223> cloning primer

<400> 69

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<210> 72

<211> 29

<212> DNA

<213> artificial

<220>

<223> cloning primer

<400> 72

tggcaggcgc gcctcagtca gcgctctcg

29

<210> 73

<211> 29

<212> DNA

<213> artificial

<220>

<223> cloning primer

<400> 73

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29

<210> 74

<211> 26

<212> DNA

<213> artificial

<220>

GFI-108 Sequence listing.ST25

<223> cloning primer

<400> 74

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26

<210> 75

<211> 25

<212> DNA

<213> artificial

<220>

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<222> (17)..(17)

<223> wherein "n" is equal to "a" or "t" or "g" or "c".

<220>

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<222> (20)..(20)

<223> wherein "n" is equal to "a" or "t" or "g" or "c".

<400> 75

cagtgaaaat acctggncn gtcca

25

<210> 76

<211> 27

<212> DNA

<213> artificial

<220>

<223> cloning primer

<400> 76

tgcctatcttt taggtccagg cccgttc

27

<210> 77

<211> 27

<212> DNA

<213> artificial

<220>

<223> cloning primer

<400> 77

gatcccacga cgcacgtat ttctttc

27

<210> 78

<211> 35

<212> DNA

<213> artificial

<220>

<223> cloning primer

<400> 78

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35

GFI-108 Sequence listing.ST25

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GFI-108 Sequence listing.ST25

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<210> 89
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GFI-108 Sequence listing.ST25

<220> cloning primer
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<210> 90
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<400> 90
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<210> 91
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<212> DNA
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<400> 91
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<210> 92
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<212> DNA
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<400> 92
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<210> 93
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<400> 93
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GFI-108 Sequence listing.ST25

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<210> 96
<211> 39
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<220>
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<400> 96
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<210> 97
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<212> DNA
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<400> 97
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<210> 98
<211> 36
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<220>
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<400> 98
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<212> DNA
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<220>
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<400> 99
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<210> 100
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GFI-108 Sequence listing.ST25

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<220>
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37